Unacceptable Jessica

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Follow up on DNA contamination of COVID-19 injectable products

It's worse than originally thought based on new results...

Jessica Rose
Mar 9

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My friend Kevin McKernan has done an incredible amount of work that has allowed the discovery of contamination in the form of dsDNA in both the Pfizer and Moderna products. You can read about that here and here. But it turns out following further and more in-depth inquiries, that it's worse than originally thought. Please refer to Anandamide's most recent Substack piece entitled: "Pfizer and Moderna bivalent vaccines contain 20-35% expression vector and are transformation competent in E.coli".

Take Home Message: The left-over expression vectors used to manufacture the mRNAs are at contamination levels 100-fold higher than originally proposed and imply trillions of DNA molecules per dose. This has implications for integration into our genome.

Implications for integration into our genome?

Wait now. Didn't they pinky-finger promise that that was impossible with a side of 'you're a moron?' and/or 'you're fired'?

Do I hear the Precautionary Principle riding in on its white steed? Nope. Just the Pfizer/Moderna/FDA/CDC/ETC trains railroading the truth.

http://www.gatewaynmra.org/get-started/

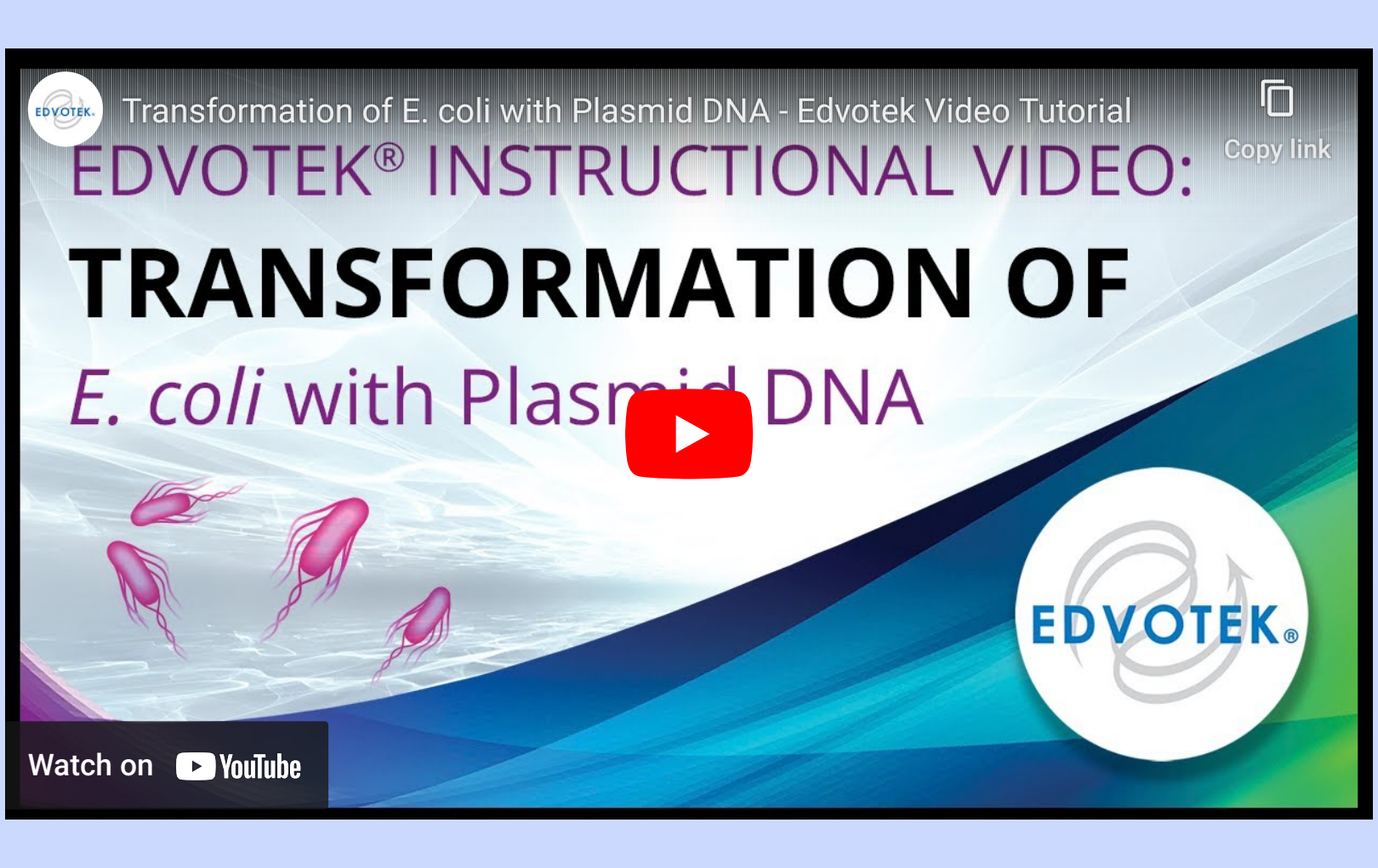
Kevin's team originally used a technique called RNA-seq to investigate whether or not there was contamination in the Pfizer and Moderna products and found high levels of kanamycin/neomycin/spike-containing expression plasmids - 'levels that exceeded the EMA specified dsDNA limits for these COVID-19 injectable products in the case of the Pfizer products'. Concerning. Very concerning. But listen to this. As part of the RNA-seq process, an additive called called actinomycin D (like Furious D) is used, and it can function to suppress DNA amplification by suppressing DNA dependent RNA polymerase activity.[1] Hmm. So doesn't that mean that there might be even more DNA than originally thought?

To check this, and to get around the potential problem of actinomycin D activities associated with RNA-seq, they decided use quantitative PCR (qPCR) and gel visualization (eletrophoresis) to get a better idea of just how much DNA contamination they were dealing with. They got rid of the mRNA from the Pfizer and Moderna samples altogether, purified the existing DNA, and used it in follow-up assays. Doing this allowed them to answer questions relating to whether or not the DNA contaminating the samples were circular or linear: ie - replication competent or not, and to assess the ratio of circular to linear DNA contaminants.

> The initial sequencing of the mRNA vaccines did not sequence deeply enough to ascertain the completeness of the linearization reaction.

This was a very important issue to address since the knee-jerk reaction to their original findings was that the DNA was linear(ized) and thus not replication competent. So, no problem! But, even if we are looking at linear plasmids (as opposed to circular), and even though the former might not be replication competent (or less than their circular mates), Kevin's team's previous estimate of billions of potentially contaminating DNA molecules is still super concerning. Why? Because the linearization reactions are likely not 100% efficient. For example, if the reactions are 99% efficient, there would still potentially be millions of replication competent plasmids present. Can you see the problem?

So the brilliant labbies got some Pfizer and Moderna samples, got rid of the modified mRNA, took out the DNA (which shouldn't be there in the first place), and then tried to transform *E. coli* bacteria using this DNA. We talked about this here but here's a refresher video: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The thing about this is that they shouldn't be finding any colonies growing at all. The fact that these plasmids are replication-competent (whatever form they take) - even in lab *E. coli* - in the first place, is concerning.

Then they did qPCR assays using specially-designed primers to amplify the spike, kan or mRNA in the plasmids, in order to estimate the plasmid to mRNA ratio.

> qPCR primers were designed using IDTs Primer Quest software targeting the Kanamycin gene in the plasmid (HEX) and the Spike protein in the plasmid and the mRNA (FAM).

This is a preferable technique to RNA-seq since the latter biases toward RNA during the sequence read.

They also ran the purified DNA and RNA products from the Pfizer and Moderna samples on gels to estimate the relative amounts and size of each nucleic acid. Always good practice to check what you're working with.

And finally they did whole genome shotgun sequencing of the DNA. It's called shotgun sequencing because - like when a shotgun is fired, the shell breaks up into lots of smaller bits - a large genetic sequence is broken up into many smaller fragments (reads) and then reassembled to match a reference sequence, as part of this sequencing technique.[2] This allowed for a more pinpointed focus on the plasmid and far higher coverage - an increase from 500-4000 (which is sufficient to determine the species or strain of the organism where the DNA comes from) up to 2 million-fold coverage!

Efficient.

So the first thing everyone should understand is that the original source of contamination is likely at the *in vitro* transcription step of production of mRNA whereby residual plasmid DNA might be left behind in the Pfizer or Moderna mRNAs. Kevin explains this well in his Substack. Here's a screenshot from his article to illustrate where and how the DNA might get left behind in the manufacturing process. What's really alarming here is that this method can also lead to truncated mRNA synthesis as I have written about extensively and also presented recently at a conference.

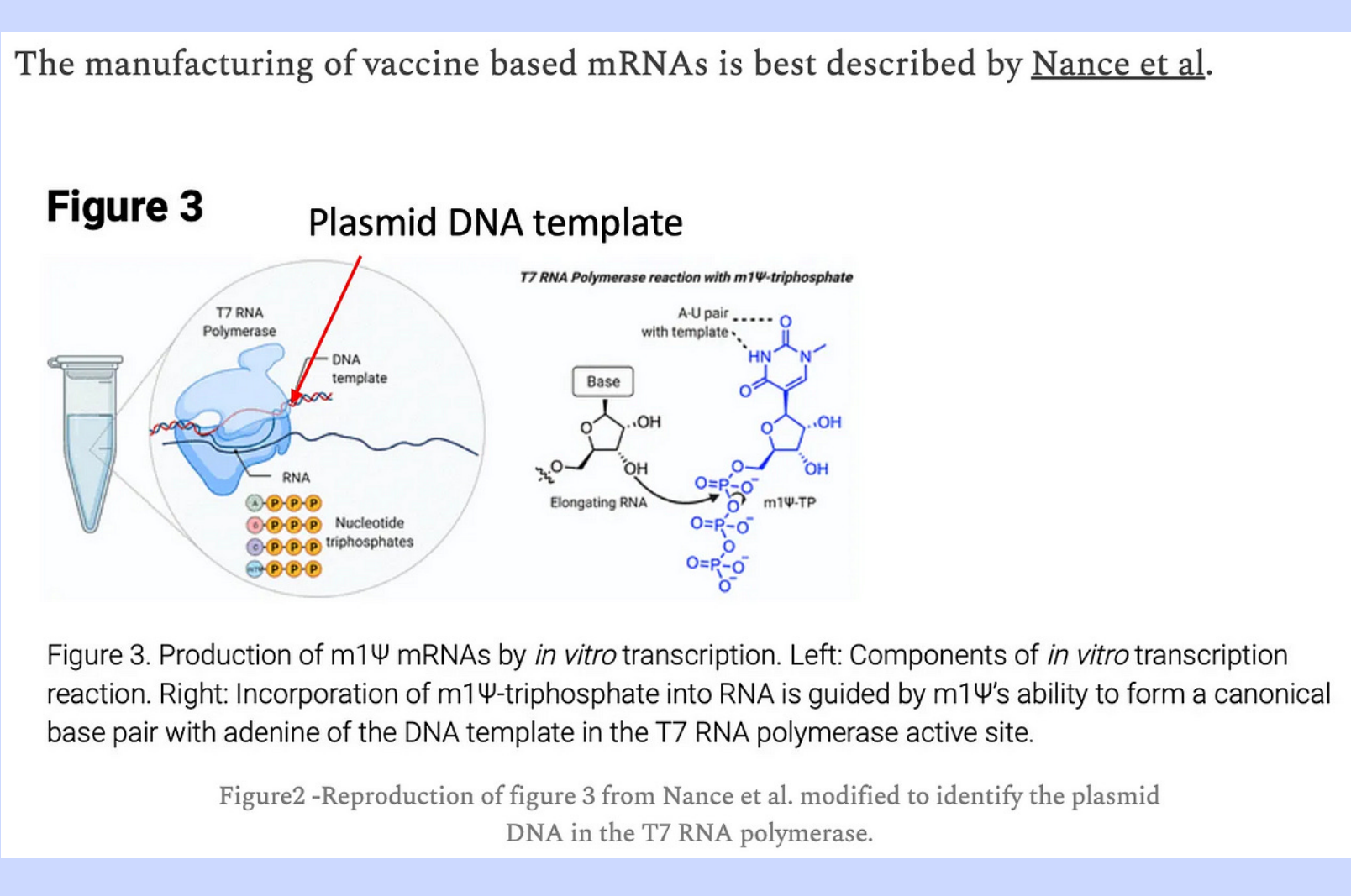
The manufacturing of vaccine based mRNAs is best described by Nance et al.

Figure 3. Production of m1Ψ mRNAs by *in vitro* transcription. Left: Components of *in vitro* transcription reaction. Right: Incorporation of m1Ψ-triphosphate into RNA is guided by m1Ψ's ability to form a canonical base pair with adenine of the DNA template in the T7 RNA polymerase active site.

Figure2 -Reproduction of figure 3 from Nance et al. modified to identify the plasmid DNA in the T7 RNA polymerase.

And as Kevin points out:

> The presence of *E.coli* based plasmids is a canary for Lipopolysaccharide (LPS or endotoxin) contamination. Whenever you see high levels of plasmid contamination derived from gram negative bacteria like *E.coli*, you should expect high levels of endotoxin contamination. Injecting endotoxin can lead to anaphylaxis and toxic shock syndrome.

THE POLICE Canary in a Coalmine
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Watch on YouTube

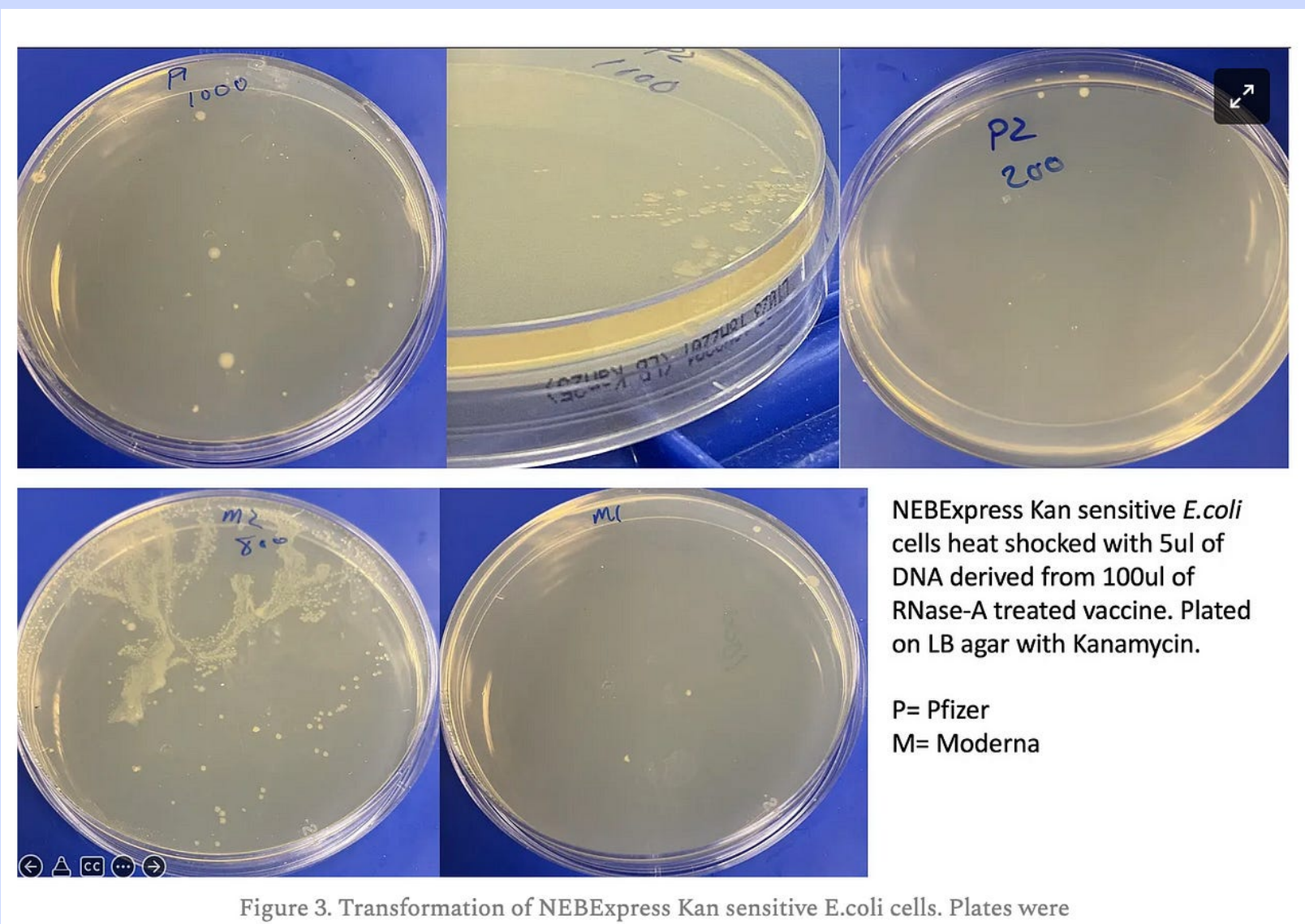
> "Your sensibilities are shaken by the slightest defect." "You say you want to spend the winter in Firenza. You so afraid to catch a dose of influenza. You live your life like a canary in a coalmine. You get so dizzy even walkin' in a straight line." The Police

By the way, where have I heard about anaphylaxis and TSS before?

I think what's the most alarming to me about what they found in this further investigation is evidence that the poly-A tails are added after mRNA synthesis. The reason I find this horrifying is because those poly-A tails could be added to well, (theoretically) anything, including truncated mRNAs. Remember we talked about this? This means that those shorter proteins we were talking about that potentially were the reason we saw smears of smaller proteins on Western Blots, are probably a very real thing. We have no idea what the physiological effects of these truncated proteins are.

Moving on…

They found gorgeous colonies in the case of both the Pfizer and Moderna-derived DNA transformations. These are Kan plates (agar infused with kanamycin antobiotic) meaning the plasmids from both the Pfizer and Moderna products conferred kanamycin resistance to the *E. coli*. That's why they grew! Lucky duckies.



NEBExpress Kan sensitive *E.coli* cells heat shocked with 5ul of DNA derived from 100ul of RNase-A treated vaccine. Plated on LB agar with Kanamycin.

P= Pfizer
M= Moderna

Figure 3. Transformation of NEBExpress Kan sensitive E.coli cells. Plates were grown at 37C for 48 hours. 200ul and 800ul of SOC were plated in order to capture the entire transformation on 1 plate.

Ultimately this means that the 'responsible' plasmids are (likely) circular and replication competent.

> An unknown portion of these dsDNA contaminants are replication competent plasmids that can transform *E.coli* with a simple 20 second 42C heat shock treatment. These plasmids provide antibiotic resistance on LB-Kan plates and can be isolated from *E.coli* cultures.

An interesting point here is the question of whether or not the 'responsible' plasmids will express spike in non-lab *E. coli*. The answer is likely 'no', since the mRNA in the Pfizer and Moderna products are specifically designed to target ribosomes for translation in mammals. The plasmids would have to be integrated into the human genome in order for the mRNA to become an issue, biologically-speaking.

Kevin writes:

> This may enable mRNA to be expressed from these plasmids in mammalian cells but unless the plasmids are integrated into the human genome, they are unlikely to be replicated to high copy number.

Very quick and dirty summary of a couple results:

RT-qPCR showed amplification of DNA of the Pfizer spike and Pfizer kan/vector at near equivalency.

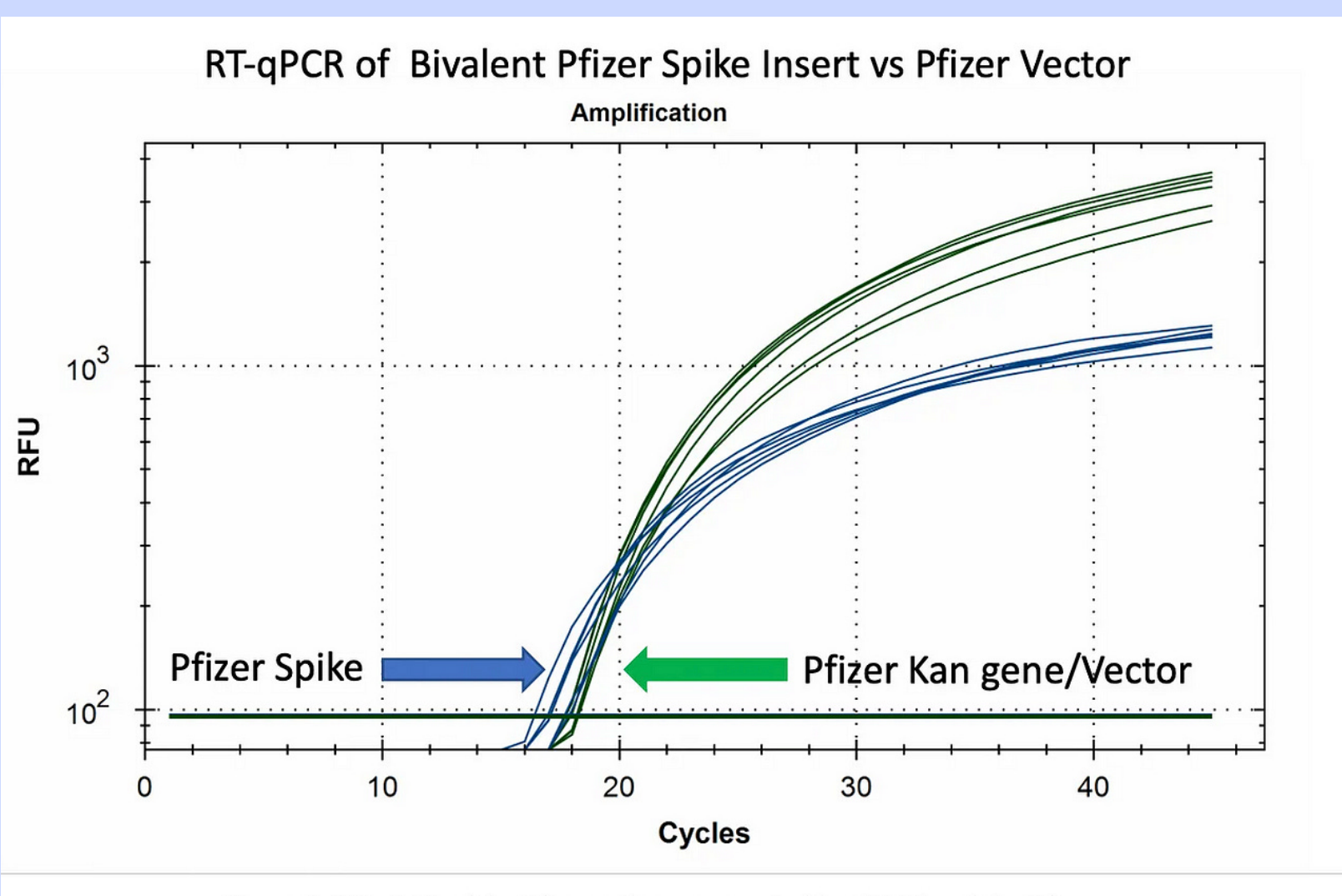


Figure 9. RT-qPCR of the Pfizer spike sequence in blue (FAM) and the Pfizer Kanamycin gene in the plasmid in Green (HEX). Near equivalent CT scores for the vector and the spike sequence imply lots of contaminating vector.

This means there's likely leurts of vector contamination. And it *is* DNA contamination that is likely very high because the CTs used in these assays were pretty low - starting below 20. For context, for all those BS PCR 'texts' they forced on everyone (and still are) they often used a cut-off of 45.

Eastern Health 45 Cycles
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Feel free to download the above for use in affidavits.

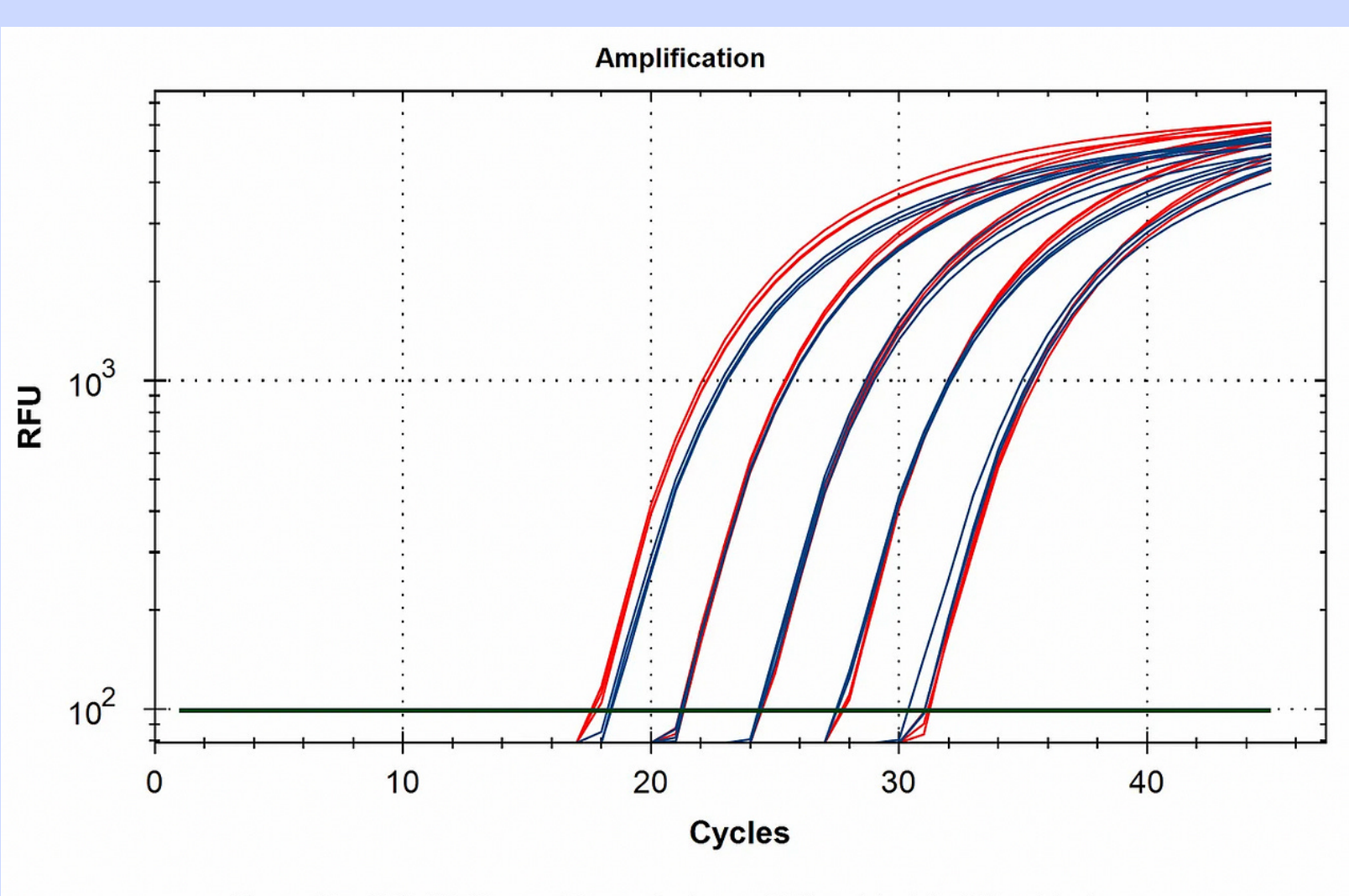

Figure 10. qPCR (No Reverse Transcription so DNA only) of the Pfizer bivalent vaccine with a multiplex qPCR assay that targets Kanamycin gene in the vector (red) and the Spike protein also in the vector (Blue). 10 Fold serial dilutions are performed in triplicate for each dilution. This assay only amplifies DNA in the vaccines and it CTs under 20 demonstrate high levels of DNA contamination.

The amount of actual contamination based on these results is likely staggering.

Kevin writes:

> The DNA contamination ranges from 8.19-11.3 ng/ul with 23-55ng/ul of mRNA. This equates to 20-35% of the nucleic acid in each vaccine being expression vector. This is several orders of magnitude over the the EMAs limit of 330ng/mg.
>
> With these levels of contamination, RT activity from LINE-1 is not a prerequisite for genome integration.

Remember all my talk about LINE-1 as the reverse transcriptase required for reverse transcription with the subsequent worry about integration of foreign DNA into our genome? Well what Kevin is saying here is that the levels of contamination of foreign DNA are so high that we don't even need to consider the problem of mRNA being reverse transcribed to DNA (poised for integration).

Ruh Roh.

Final remarks from a truly diligent scientist:

> These data cannot inform on genome integration and further IRB reviewed deep sequencing work is required to address rare mosaic integration events in patients. Regardless of these hypothetical concerns, the dsDNA contamination exceeds the EMA specifications by several orders of magnitude and further scrutiny should be applied to the endotoxin levels and dsRNA levels in these vaccines.

The real life health problems that millions of humans are experiencing following being coerced (in the majority of cases) into being injected with this garbage are plentiful and wide-ranging. It is more than likely that these adverse effects are the direct result of the contamination illuminated by Kevin and his team. And by the way, the techniques that Kevin used to reach these conclusions are *very* common and furthermore, no great cost or expertise are required to use them.

Take home message: Why were these basic assays/procedures not done/carried out prior to injecting billions of people? Or at least, somewhere along the way? Why were my colleagues being threatened for sequencing the crap in the Pfizer and Moderna vials?

I think the answer is very clear: they were afraid of what would be found. Not just as per the sequences themselves (ie: furin-cleavage, HIV and cutting sites), but as per contamination arising in the production of the mRNA used in every shot.

Sorry if there are typos or a lack of flow in this piece. I got entirely distracted and swept away by The Police in the final proofread. I got dizzy walkin' in a straight line. :)

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[1] Wendolyn R. Davis, Sam Gabbara, Donald Hupe, and James A. Peliska. Actinomycin D Inhibition of DNA Strand Transfer Reactions Catalyzed by HIV-1 Reverse Transcriptase and Nucleocapsid Protein. *Biochemistry* 1998, 37, 40, 14213–14221. Publication Date: September 17, 1998. https://doi.org/10.1021/bi9814890

[2] https://bitesizebio.com/31257/introduction-shotgun-sequencing/

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EdWrites We love mythsMar 9

> ... [something] used to manufacture [the vaccine] are at contamination levels 100-fold higher than originally proposed and imply trillions of DNA molecules per dose...

We have left the tip of the iceberg and are now coming down below the surface of water. Let's recap. This vaccine was widely promised to be the most transparent event in the history of mankind. (Obviously, 75 years came up only because of the size of the material to be disclosed, no other factors, right?) It has been accepted by default as "safe and effective" to the degree that justified skipping all crucial components of testing before opening Phase 1. (Assuming that they were really trying to do something good for humanity.) It has been presented as "no other option" in the opinion of our saviors. And it has been incentivized as "free" (in the sense that Madoff and Ponzi should be worshipped as angels). Cutting corners was packaged into "ah, we've been working on some aspects for a long time" or "we separated the process into parallel tracks", depending what was more comfortable at the time. Despite the fact that the reverse of medical knowledge was (still is?) that there is no possibility to create a preventive measure for coronaviruses. As greatly proven by negative efficiency of flu vaccines.

Now we have a signal indicating the inability to control the manufacturing process sufficiently enough to ensure purity of the final product (covid vaccine). Shouldn't it warrant an immediate shutdown of the manufacturing sites? And ultra-strict audits?

We also have a signal that uniform composition of this vaccine across retailer batches cannot be maintained. Shouldn't it warrant an immediate... see above.

But there is more.

If this high-profile vaccine, definitely the most expensive medical product in the history, is so

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Dr Ah Kahn Syed Writes Arkmedic's blogMar 9 Liked by Jessica Rose

And of course this pushes those "not gene therapy (but are anyway)" gene therapies straight into GMO land, no question. Which then makes all those drug regulator approvals illegal.

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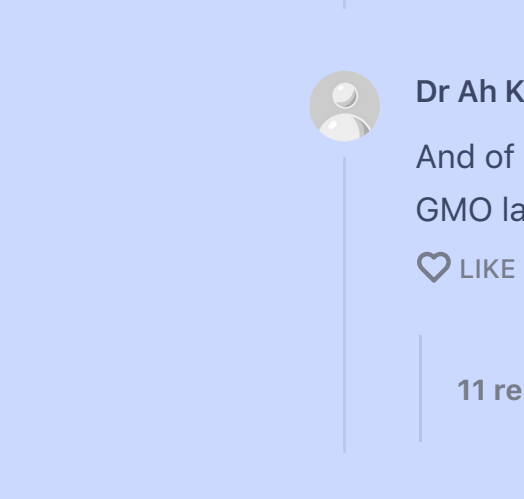

This is one of the emails I received the other day. I get hundreds daily, and I am hearing you all.
This particular note spoke loudly to me and this lovely person gave me permission to share her words.
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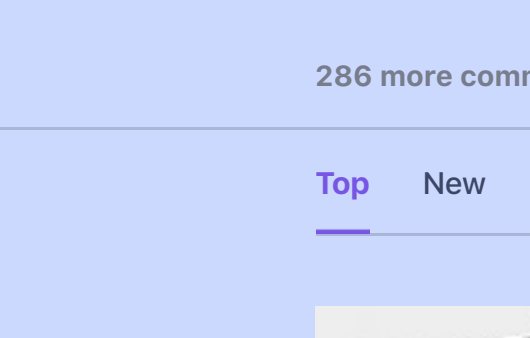

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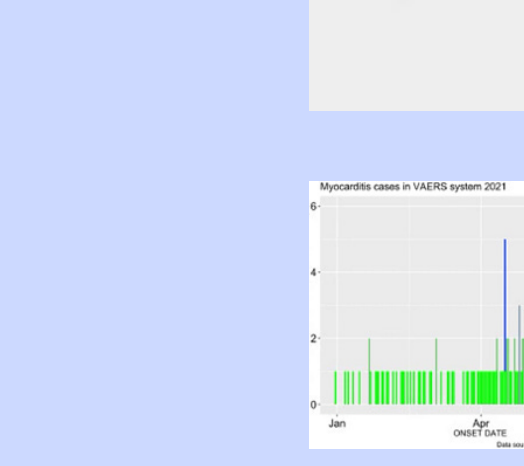

Rewrite: Let's tag team this until everybody understands
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